Amendments to the Specification:

Please replace the paragraph beginning at page 35, line 7, with the following rewritten paragraph:

Nucleotide sequences of the instantly-described nucleic acids were determined by sequencing a DNA molecule that had resulted, directly or indirectly, from at least one enzymatic polymerization reaction (e.g., reverse transcription and/or polymerase chain reaction) using an automated sequencer (such as the ~~MegaBACE™~~ MEGABACE™ 1000, Molecular Dynamics, Sunnyvale, CA, USA). Further, all amino acid sequences of the polypeptides of the present invention were predicted by translation from the nucleic acid sequences so determined, unless otherwise specified.

Please replace the paragraph beginning at page 36 line 4, with the following rewritten paragraph:

Commercially available fluorescent nucleotide analogues readily incorporated into the nucleic acids of the present invention include Cy3-dCTP, Cy3-dUTP, Cy5-dCTP, Cy3-dUTP (Amersham Pharmacia Biotech, Piscataway, New Jersey, USA), fluorescein-12-dUTP, tetramethylrhodamine-6-dUTP, Texas Red ®-5-dUTP, Cascade Blue ®-7-dUTP, BODIPY ® FL-14-dUTP, BODIPY ® TMR-14-dUTP, BODIPY ® TR-14-dUTP, ~~Rhodamine Green~~ RHODAMINE

GREEN™-5-dUTP, Oregon Green ® 488-5-dUTP, Texas Red ®-12-dUTP, BODIPY ® 630/650-14-dUTP, BODIPY ® 650/665-14-dUTP, Alexa Fluor ® 488-5-dUTP, Alexa Fluor ® 532-5-dUTP, Alexa Fluor ® 568-5-dUTP, Alexa Fluor ® 594-5-dUTP, Alexa Fluor ® 546-14-dUTP, fluorescein-12-UTP, tetramethylrhodamine-6-UTP, Texas Red ®-5-UTP, Cascade Blue ®-7-UTP, BODIPY ® FL-14-UTP, BODIPY ® TMR-14-UTP, BODIPY ® TR-14-UTP, ~~Rhodamine Green~~ RHODAMINE GREEN™-5-UTP, Alexa Fluor ® 488-5-UTP, Alexa Fluor ® 546-14-UTP (Molecular Probes, Inc. Eugene, OR, USA). One may also custom synthesize nucleotides having other fluorophores. See Henegariu et al., Nature Biotechnol. 18: 345-348 (2000), the disclosure of which is incorporated herein by reference in its entirety.

Please replace the paragraph beginning at page 37, line 3, with the following rewritten paragraph:

Other post-synthetic approaches also permit internal labeling of nucleic acids. For example, fluorophores can be attached using a cisplatin reagent that reacts with the N7 of guanine residues (and, to a lesser extent, adenine bases) in DNA, RNA, and PNA to provide a stable coordination complex between the nucleic acid and fluorophore label (Universal Linkage System) (available from Molecular Probes, Inc., Eugene, OR, USA and

Amersham Pharmacia Biotech, Piscataway, NJ, USA); see Alers et al., Genes, Chromosomes & Cancer 25: 301- 305 (1999); Jelsma et al., J. NIH Res. 5: 82 (1994); Van Belkum et al., BioTechniques 16: 148-153 (1994), incorporated herein by reference. As another example, nucleic acids can be labeled using a disulfide-containing linker (~~FastTag~~ FASTTAG™ Reagent, Vector Laboratories, Inc., Burlingame, CA, USA) that is photo- or thermally-coupled to the target nucleic acid using aryl azide chemistry; after reduction, a free thiol is available for coupling to a hapten, fluorophore, sugar, affinity ligand, or other marker.

Please replace the paragraph beginning at page 48, line 25, with the following rewritten paragraph:

Expression control sequences for yeast cells, typically S. *cerevisiae*, will include a yeast promoter, such as the CYC1 promoter, the GAL1 promoter, the GAL10 promoter, ADH1 promoter, the promoters of the yeast ~~mating~~ α-mating system, or the GPD promoter, and will typically have elements that facilitate transcription termination, such as the transcription termination signals from the CYC1 or ADH1 gene.

Please replace the paragraph beginning at page 51, line 9, with the following rewritten paragraph:

Vectors for phage display fuse the encoded polypeptide to, e.g., the gene III protein (pIII) or gene VIII protein (pVIII) for display on the surface of filamentous phage, such as M13. See Barbas et al., Phage Display: A Laboratory Manual, Cold Spring Harbor Laboratory Press (2001); Kay et al. (eds.), Phage Display of Peptides and Proteins: A Laboratory Manual, Academic Press, Inc., (1996); Abelson et al. (eds.), Combinatorial Chemistry (Methods in Enzymology, Vol. 267) Academic Press (1996). Vectors for yeast display, e.g. the pYD1 yeast display vector (Invitrogen, Carlsbad, CA, USA), use the ~~agglutinin~~ α-agglutinin yeast adhesion receptor to display recombinant protein on the surface of S. *cerevisiae*. Vectors for mammalian display, e.g., the ~~pDisplay~~ PDISPLAY™ vector (Invitrogen, Carlsbad, CA, USA), target recombinant proteins using an N-terminal cell surface targeting signal and a C-terminal transmembrane anchoring domain of platelet derived growth factor receptor.

Please replace the paragraph beginning at page 53, line 10, with the following rewritten paragraph:

Replication incompetent retroviral vectors, typically derived from Moloney murine leukemia virus, also are useful for creating stable transfectants having integrated provirus. The highly efficient transduction machinery of retroviruses, coupled with the availability of a variety of packaging cell lines such as ~~RetroPack~~ RETROPACK™ PT 67, ~~EcoPack2~~ ECOPACK2™-293, AmphoPack-293, and GP2-293 cell lines (all available from Clontech Laboratories, Palo Alto, CA, USA), allow a wide host range to be infected with high efficiency; varying the multiplicity of infection readily adjusts the copy number of the integrated provirus.

Please replace the paragraph beginning at page 54, line 3, with the following rewritten paragraph:

Polypeptides of the invention may be post-translationally modified. Post-translational modifications include phosphorylation of amino acid residues serine, threonine and/or tyrosine, N-linked and/or O-linked glycosylation, methylation, acetylation, prenylation, methylation, acetylation, arginylation, ubiquination and racemization. One may determine whether a

polypeptide of the invention is likely to be post-translationally modified by analyzing the sequence of the polypeptide to determine if there are peptide motifs indicative of sites for post-translational modification. There are a number of computer programs that permit prediction of post-translational modifications. See, e.g., ~~www.expasy.org~~ expasy with the extension .org of the world wide web (accessed August 31, 2001), which includes PSORT, for prediction of protein sorting signals and localization sites, SignalP, for prediction of signal peptide cleavage sites, MITOPROT and Predotar, for prediction of mitochondrial targeting sequences, NetOGlyc, for prediction of type O-glycosylation sites in mammalian proteins, big-PI Predictor and DGPI, for prediction of prenylation-anchor and cleavage sites, and NetPhos, for prediction of Ser, Thr and Tyr phosphorylation sites in eukaryotic proteins. Other computer programs, such as those included in GCG, also may be used to determine post-translational modification peptide motifs.

Please replace the paragraph beginning at page 54, line 20, with the following rewritten paragraph:

General examples of types of post-translational modifications may be found in web sites such as the Delta Mass

database ~~http://www.abrf.org/ABRF/Research Committees/deltamass/deltamass.html~~ abrf with the extension .org/ABRF/Research Committees/deltamass/deltamass.html of the world wide web(accessed October 19, 2001); "GlycoSuiteDB: a new curated relational database of glycoprotein glycan structures and their biological sources" Cooper et al. Nucleic Acids Res. 29; 332-335 (2001) and ~~http://www.glycosuite.com/~~ glycosuite with the extension .com/ of the world wide web (accessed October 19, 2001); "O-GLYCBASE version 4.0: a revised database of O-glycosylated proteins" Gupta et al. Nucleic Acids Research, 27: 370-372 (1999) and ~~http://www.cbs.dtu.dk/databases/OGLYCBASE/~~ cbs with the extension .dtu.dk/databases/OGLYCBASE/ of the world wide web(accessed October 19, 2001); "PhosphoBase, a database of phosphorylation sites: release 2.0.", Kreegipuu et al. Nucleic Acids Res 27(1):237-239 (1999) and ~~http://www.cbs.dtu.dk/databases/PhosphoBase/~~ cbs with the extension .dtu.dk/databases/PhosphoBase/ of the world wide web(accessed October 19, 2001); or ~~http://pir.georgetown.edu/ pirwww/search/textresid.html~~ pir with the extension .georgetown.edu/pirwww/search/textresid.html of world wide web(accessed October 19, 2001).

Please replace the paragraph beginning at page 56, line 25, with the following rewritten paragraph:

In another embodiment, the invention provides polypeptides that have been post-translationally modified. In one embodiment, polypeptides may be modified enzymatically or chemically, by addition or removal of a post-translational modification. For example, a polypeptide may be glycosylated or deglycosylated enzymatically. Similarly, polypeptides may be phosphorylated using a purified kinase, such as a MAP kinase (e.g, p38, ERK, or JNK) or a tyrosine kinase (e.g., Src or erbB2). A polypeptide may also be modified through synthetic chemistry. Alternatively, one may isolate the polypeptide of interest from a cell or tissue that expresses the polypeptide with the desired post-translational modification. In another embodiment, a nucleic acid molecule encoding the polypeptide of interest is introduced into a host cell that is capable of post-translationally modifying the encoded polypeptide in the desired fashion. If the polypeptide does not contain a motif for a desired post-translational modification, one may alter the post-translational modification by mutating the nucleic acid sequence of a nucleic acid molecule encoding the polypeptide so that it contains a site for the desired post-translational

modification. Amino acid sequences that may be post-translationally modified are known in the art. See, e.g., the programs described above on the website ~~www.expasy.org~~ expasy with the extension .org of the world wide web. The nucleic acid molecule is then ~~be~~ introduced into a host cell that is capable of post-translationally modifying the encoded polypeptide. Similarly, one may delete sites that are post-translationally modified by either mutating the nucleic acid sequence so that the encoded polypeptide does not contain the post-translational modification motif, or by introducing the native nucleic acid molecule into a host cell that is not capable of post-translationally modifying the encoded polypeptide.

Please replace the paragraph beginning at page 58, line 16, with the following rewritten paragraph:

A wide variety of unicellular host cells are useful in expressing the DNA sequences of this invention. These hosts may include well-known eukaryotic and prokaryotic hosts, such as strains of, fungi, yeast, insect cells such as Spodoptera frugiperda (SF9), animal cells such as CHO, as well as plant cells in tissue culture. Representative examples of appropriate host cells include, but are not limited to, bacterial cells, such

as E. *coli*, *Caulobacter crescentus*, *Streptomyces* species, and *Salmonella typhimurium*; yeast cells, such as *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Pichia pastoris*, *Pichia methanolica*; insect cell lines, such as those from *Spodoptera frugiperda*, e.g., Sf9 and Sf21 cell lines, and ~~expresSF~~ EXPRESSF™ cells (Protein Sciences Corp., Meriden, CT, USA), *Drosophila* S2 cells, and *Trichoplusia ni* High Five ® Cells (Invitrogen, Carlsbad, CA, USA); and mammalian cells. Typical mammalian cells include BHK cells, BSC 1 cells, BSC 40 cells, BMT 10 cells, VERO cells, COS1 cells, COS7 cells, Chinese hamster ovary (CHO) cells, 3T3 cells, NIH 3T3 cells, 293 cells, HEPG2 cells, HeLa cells, L cells, MDCK cells, HEK293 cells, WI38 cells, murine ES cell lines (e.g., from strains 129/SV, C57/BL6, DBA-1, 129/SVJ), K562 cells, Jurkat cells, and BW5147 cells. Other mammalian cell lines are well-known and readily available from the American Type Culture Collection (ATCC) (Manassas, VA, USA) and the National Institute of General Medical Sciences (NIGMS) Human Genetic Cell Repository at the Coriell Cell Repositories (Camden, NJ, USA). Cells or cell lines derived from breast are particularly preferred because they may provide a more native post-translational processing. Particularly preferred are human

breast cells.

Please replace the paragraph beginning at page 59, line 20, with the following rewritten paragraph:

Plasmid vectors will typically be introduced into chemically competent or electroccompetent bacterial cells. E. *coli* cells can be rendered chemically competent by treatment, e.g., with $CaCl_2$, or a solution of Mg^{2+}, Mn^{2+}, Ca^{2+}, Rb^{+} or K^{+}, dimethyl sulfoxide, dithiothreitol, and hexamine cobalt (III), Hanahan, J. Mol. Biol. 166(4):557-80 (1983), and vectors introduced by heat shock. A wide variety of chemically competent strains are also available commercially (e.g., Epicurian Coli ® XL10-Gold ® Ultracompetent Cells (Stratagene, La Jolla, CA, USA); DH5 competent cells (Clontech Laboratories, Palo Alto, CA, USA); and TOP10 Chemically Competent E. *coli* Kit (Invitrogen, Carlsbad, CA, USA)). Bacterial cells can be rendered electrocompetent, that is, competent to take up exogenous DNA by electroporation, by various pre-pulse treatments; vectors are introduced by electroporation followed by subsequent outgrowth in selected media. An extensive series of protocols is provided online in Electroprotocols (BioRad, Richmond, CA, USA) (~~http://www.biorad.com/LifeScience/pdf/ New_Gene_Pulser.pdf~~

biorad with the extension .com/LifeScience/pdf/ New_Gene_Pulser.pdf of the world wide web).

Please replace the paragraph beginning at page 60, line 25, with the following rewritten paragraph:

Mammalian and insect cells can be directly infected by packaged viral vectors, or transfected by chemical or electrical means. For chemical transfection, DNA can be coprecipitated with $CaPO_4$ or introduced using liposomal and nonliposomal lipid-based agents. Commercial kits are available for $CaPO_4$ transfection (~~CalPhos~~ CALPHOS™ Mammalian Transfection Kit, Clontech Laboratories, Palo Alto, CA, USA), and lipid-mediated transfection can be practiced using commercial reagents, such as LIPOFECTAMINE™ 2000, LIPOFECTAMINE™ Reagent, CELLFECTIN ® Reagent, and LIPOFECTIN ® Reagent (Invitrogen, Carlsbad, CA, USA), DOTAP Liposomal Transfection Reagent, FuGENE 6, X-tremeGENE Q2, DOSPER, (Roche Molecular Biochemicals, Indianapolis, IN USA), Effectene™, PolyFect ®, Superfect ® (Qiagen, Inc., Valencia, CA, USA). Protocols for electroporating mammalian cells can be found online in Electroprotocols (Bio-Rad, Richmond, CA, USA) (~~http://www.bio-rad.com/LifeScience/pdf/ New_Gene_Pulser.pdf~~ bio-rad with the extension .com/LifeScience/pdf/

New_Gene_Pulser.pdf of the world wide web); Norton et al. (eds.), Gene Transfer Methods: Introducing DNA into Living Cells and Organisms, BioTechniques Books, Eaton Publishing Co. (2000); incorporated herein by reference in its entirety. Other transfection techniques include transfection by particle bombardment and microinjection. *See, e.g.*, Cheng et al., *Proc. Natl. Acad. Sci.* USA 90(10): 4455-9 (1993); Yang et al., *Proc. Natl. Acad. Sci.* USA 87(24): 9568-72 (1990).

Please replace the paragraph beginning at page 75, line 12, with the following rewritten paragraph:

Fusion partners include, *inter alia*, *myc*, hemagglutinin (HA), GST, immunoglobulins, β-galactosidase, biotin trpE, protein A, β-lactamase, ~~amylase~~ α-amylase, maltose binding protein, alcohol dehydrogenase, polyhistidine (for example, six histidine at the amino and/or carboxyl terminus of the polypeptide), lacZ, green fluorescent protein (GFP), yeast ~~mating~~ α-mating factor, GAL4 transcription activation or DNA binding domain, luciferase, and serum proteins such as ovalbumin, albumin and the constant domain of IgG. *See, e.g.*, Ausubel (1992), *supra* and Ausubel (1999), *supra*. Fusion proteins may also contain sites for

specific enzymatic cleavage, such as a site that is recognized by enzymes such as Factor XIII, trypsin, pepsin, or any other enzyme known in the art. Fusion proteins will typically be made by either recombinant nucleic acid methods, as described above, chemically synthesized using techniques well-known in the art (e.g., a Merrifield synthesis), or produced by chemical cross-linking.

Please add the following new paragraphs at page 118, line 16:

--**Example 1a: Suppression subtractive hybridization (Clontech PCR-SELECT)**

Clontech PCR-SELECT is a PCR based subtractive hybridization method designed to selectively enrich for cDNAs corresponding to mRNAs differentially expressed between two mRNA populations (Diatchenko *et al, Proc. Natl. Acad. Sci. USA*, Vol. 93, pp. 6025-6030, 1996).

Clontech PCR-SELECT is a method for enrichment of differentially expressed mRNAs based on a selective amplification. cDNA is prepared from the two mRNA populations which are to be compared (Tester: cDNA population in which the differentially expressed messages are sought and Driver: cDNA

population in which the differentially expressed transcripts are absent or low). The tester sample is separated in two parts and different PCR adapters are ligated to the 5′ ends. Each tester is separately annealed to excess driver (first annealing) and then pooled and again annealed (second annealing) to excess driver. During the first annealing, sequences common to both populations anneal. Additionally the concentration of high and low abundance messages are normalized since annealing is faster for abundant molecules due to the second order kinetics of hybridization. During the second annealing cDNAs unique or overabundant to the tester can anneal together. Such molecules have different adapters at their ends. The addition of additional driver during the second annealing enhances the enrichment of the desired differentially expressed sequences. During subsequent PCR, molecules that have different adapters at each end amplify exponentially. Molecules which have identical adapters, or adapters at only one end, or no adapters (driver sequences) either do not amplify or undergo linear amplification. The end result is enrichment for cDNAs corresponding to differentially expressed messages (unique to the tester or upregulated in the tester). This technique was used to identify transcripts unique to lung tissues or messages overexpressed in

lung cancer tissues.

Pairs of matched samples were isolated from the same patient, a cancer sample, and the "normal" adjacent tissue from the same tissue type. The mRNA from the cancer tissue was used as the "tester", and the non-cancer mRNA as a "driver". The non-cancer "driver" is from the same individual and tissue as the cancer sample (Matched). Alternatively, the "driver" can be from a different individual but the same tissue as the tumor sample (unmatched). In some cases "driver" mixtures of mRNAs derived from non-cancer tissues types different from the cancer tissue type are used. The last approach allows the identification of transcripts whose expression is specific or upregulated in the cancer tissue type analyzed. Such transcripts may or may not be cancer specific in their expression.

Several subtracted libraries were generated for lung tissue. The product of the subtraction experiments was used to generate cDNA libraries. These cDNA libraries contain Expressed Sequence Tags (ESTs) from genes that are lung specific, or upregulated in lung tissue. Randomized clones picked from each cDNA PCR Select library were sequenced and the genes identified by a systematic analysis of the sequence data against the LIFESEQ Gold database available from Incyte Pharmaceuticals, Palo Alto. The sequences

with no significant homology to any DNA sequence present in the database are considered novel sequences. These lung cancer specific markers are DEX0123_1 through DEX0123_99 and correspond to markers of the instant sequence listing. In particular, SEQ ID NO:41 and 42 correspond to DEX0123_33 (SEQ ID NO:33).--

Please replace the paragraph beginning at page 124, line 35, with the following rewritten paragraph:

Examples of post-translational modifications (PTMs) of the LSPs of this invention are listed below. In addition, antibodies that specifically bind such post-translational modifications may be useful as a diagnostic or as therapeutic. Using the ProSite database (Bairoch et al., Nucleic Acids Res. 25(1):217-221 (1997), the contents of which are incorporated by reference), the following PTMs were predicted for the BSPs of the invention (~~http://npsa-pbil.ibcp.fr/cgi-bin/npsa_automat.pl?page=npsa_prosite.html~~ npsa-pbil with the extension .ibcp.fr/cgi-bin/npsa_automat.pl?page=npsa_prosite.html of the world wide web most recently accessed October 23, 2001).